SEQUENCE LISTING

| (1) | GENERAL | INFORMATION: |
|-------|---------|--------------|
| · - / | O + | |

| i | (i ' | APPLICANT | |
|---|-------|-----------|--|
| и | 1 . | AFFILCANI | |

- (A) NAME: Yi Sun (B) STREET: 4841 Hillway Court
- (C) CITY: Ann Arbor
 (D) STATE: Michigan
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 48105 (G) TELEPHONE: (313) 996-1959 (H) TELEFAX: (313) 996-7158
- (ii) TITLE OF INVENTION: Sensitive to Apoptosis Gene (SAG)
- (iii) NUMBER OF SEQUENCES: 50
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1140 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 17..355
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 (B) LOCATION:17..355
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...1140
 - (D) OTHER INFORMATION:/note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| GTT | CTGCC | GCC (| CCG | | rg go et Al 1 | | | | | | | | lu Pi | | | 49 |
|------------------|------------------|------------------|------------------|------------|---------------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|------------|------------------|-----|
| GTC Val | CTT Leu | TCT Ser | TCG Ser 15 | CAC His | TCC Ser | GGG Gly | AGC Ser | GCA Ala 20 | GGC Gly | TCC Ser | AAG Lys | TCG Ser | GGA Gly 25 | GGC Gly | GAC Asp | 97 |
| AAG Lys | ATG Met | TTC Phe 30 | TCT Ser | CTC Leu | AAG Lys | AAG Lys | TGG Trp 35 | AAC Asn | GCG Ala | GTA Val | GCC Ala | ATG Met 40 | TGG Trp | AGC Ser | TGG Trp | 145 |
| GAC Asp | GTT Val 45 | GAG | TGC Cys | GAT Asp | ACC Thr | TGT Cys 50 | GCC Ala | ATC Ile | TGC Cys | AGG Arg | GTC Val 55 | CAG Gln | GTG Val | ATG Met | GAT Asp | 193 |
| GCC Ala 60 | TGC Cys | CTT Leu | CGA Arg | TGT Cys | CAA Gln 65 | GCT Ala | GAA Glu | AAC Asn | AAG Lys | CAA Gln 70 | GAG Glu | GAC Asp | TGT Cys | GTT Val | GTG Val 75 | 241 |
| | | | | | AAC | | | | | | | | | | | 289 |

85

| TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val 95 100 105 | 337 |
|--|------|
| GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG Val Gln Arg Ile Gly Lys 110 | 385 |
| TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT | 445 |
| GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTTGG | 505 |
| GAAATTCTCT ACAATTAAGA TAATTTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT | 565 |
| GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC | 625 |
| CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTTTATGCT TGAGGGTTAA | 685 |
| AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT | 745 |
| AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG | 805 |
| AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG | 865 |
| GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA | 925 |
| AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTG CCGAAGGTTG | 985 |
| TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG | 1045 |
| TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC | 1105 |
| TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG | 1140 |

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His

Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp \$45\$

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

| 1 | i. | v | FEATURE: | |
|---|----|---|----------|--|
| | | | | |

- (A) NAME/KEY: CDS (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION:1..754
 (D) OTHER INFORMATION:/note= "Human SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| | | | | - | | | | | | | | | | | | | |
|---|-----------------|---------------|------------|-------------------|-----------------|------------|------------|---------------|-------------------|------------------|------------------|------------|------------|-------------------|------------------|------------|-----|
|] | ATG Met 1 | GCC Ala | GAC Asp | GTG Val | GAA Glu 5 | GAC Asp | GGA Gly | GAG Glu | GAA Glu | ACC Thr 10 | TGC Cys | GCC Ala | CTG Leu | GCC Ala | TCT Ser 15 | CAC His | 48 |
| , | TCC Ser | GGG Gly | AGC Ser | TCA Ser 20 | GGC Gly | TCC Ser | AAG Lys | TCG Ser | GGA Gly 25 | GGC Gly | GAC Asp | AAG Lys | ATG Met | TTC Phe 30 | TCC Ser | CTC Leu | 96 |
| | | | | | | | | | | | TGG Trp | | | | | | 144 |
| | | | | | | | | | | | GAT Asp | | | | | | 192 |
| | | | | | | | | | | | GTG Val 75 | | | | | | 240 |
| | | | | | | | | | | | CTG Leu | | | | | | 288 |
| į | AAT Asn | CGC Arg | TGC Cys | CCT Pro 100 | CTC Leu | TGC Cys | CAG Gln | CAG Gln | GAC Asp 105 | TGG Trp | GTG Val | GTC Val | CAA Gln | AGA Arg 110 | ATC Ile | GGC Gly | 336 |
| | AAA Lys | TGAG | GAGT | GGT 1 | raga | AGGC' | rt C | rtag(| CGCA | G TTC | GTTC2 | AGAG | CCC | rggto | GGA | | 389 |
| | TCT | rgta <i>i</i> | ATC (| CAGT | GCCC' | ra cz | AAAG | GCTA | G AA | CACT | ACAG | GGG | ATGA | TTE | CTTC | AAATAG | 449 |
| | GAG | CCGA | rgg 2 | ATCT | GTGG' | rc T | rtgg: | ACTC | A TC | AAAG | CCTT | GGT' | rage: | TTA | rgtc | AGTTTT | 509 |
| | ATC: | rtca | GAA Z | ATTC | rctg' | rg A | TAA | GAAG | A TA | ATTT | ATTA | AAG | GTGG' | rcc ' | TTCC' | PACCTC | 569 |
| | TGT | GGTG | rgt (| GTCG | CGCA | CA C | AGCT' | raga <i>i</i> | A GT | GCTA | FAAA | AAA | GGAA | AGA (| GCTC | CAAATT | 629 |
| | GAA' | rcaco | CTT I | АТАА' | TTTA | cc c | ATTT | CTAT | A CA | ACAG | GCAG | TGG | AAGC | AGT ' | rtcg/ | AGACTT | 689 |
| | TTT | CGAT | GCT ' | TATG | GTTG | AT C | AGTT | AAAA | A AG | AATG' | ГТАС | AGT | AACA | AAT A | AAAG' | rgcagt | 749 |
| | TTA | AA | | | | | | | | | | | | | | | 754 |

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 105 Lys (2) INFORMATION FOR SEQ ID NO: 5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide P1 downstream primer" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: 18 AAGCTTTTTT TTTTTTR (2) INFORMATION FOR SEQ ID NO: 6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "Oligonucleotide: P2 upstream primer" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: 13 AAGCTTNNNN NNN (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 7: | |
|------|----------|--|----|
| CGGG | GATCC | CC ATGGCCGACG TGAGG | 25 |
| (2) | INFO | RMATION FOR SEQ ID NO: 8: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| • | (ii) | MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02" | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 8: | |
| CGG | GATCC | TC ATTTGCCGAT TCTTTG | 26 |
| (2) | INFO | RMATION FOR SEQ ID NO: 9: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) | MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide P.01" | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 9: | |
| TAT | GGCTA | GC ATGGCCGACG TGGAGG | 26 |
| (2) | INFO | RMATION FOR SEQ ID NO: 10: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) | MOLECULE TYPE: peptide | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 10: | |
| | Gln 1 | Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg 5 10 15 | |
| (2) | INFO | RMATION FOR SEQ ID NO: 11: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (ii) | MOLECULE TYPE: cDNA | |
| | (ix) | FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1270 | |

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

| ATG Met 1 | GCC Ala | GAC Asp | GTG Val | GAA Glu 5 | GAC Asp | GGA Gly | GAG Glu | GAA Glu | ACC Thr 10 | TGC Cys | GCC Ala | CTG Leu | GCC Ala | TCT Ser 15 | CAC His | 48 |
|------------------|------------------|-------------|------------|-----------------|------------------|------------------|------------|------------|------------------|------------------|------------------|------------|------------|------------------|------------------|-------|
| | | | | | | | | | | | | | | | CTC Leu | 96 |
| | | | | | | | | | | | | | | | GAT Asp | 144 |
| ACG Thr | TGC Cys 50 | GCC Ala | ATC Ile | TGC Cys | AGG Arg | GTC Val 55 | CAG Gln | ATG Met | CCT Pro | GTC Val | TTA Leu 60 | GAT Asp | GTC Val | AAG Lys | CTG Leu | 192 |
| AAA Lys 65 | ACA Thr | AAC Asn | AAG Lys | AGG Arg | ACT Thr 70 | GTG Val | TTG Leu | TGG Trp | TCT Ser | GGG Gly 75 | GAG Glu | AAT Asn | GTA Val | ATC Ile | ATT Ile 80 | 240 |
| | | | ACT Thr | | | | | | | TGA | AACA | GAA (| CAAT | CGCT | GC | 290 |
| ССТ | CTCT | GCC . | AGCA | GGAC' | rg go | GTGG | rcca. | A AG | AATC | GGCA | AAT | GAGA | GTG (| GTTA | GAAGG | C 350 |
| TTC | rtag(| CGC . | AGTT | GTTC | AG A | GCCC' | rggt | G GA | rctt(| GTAA | TCC | AGTG(| ccc ' | TACA | AAGGC' | т 410 |
| AGA | ACAC | rac . | AGGG | GATG | AA T' | rctt | CAAA' | r ago | GAGC | CGAT | GGA' | rctg' | rgg ' | TCTT | rggac' | т 470 |
| CATO | CAAA | GCC ' | TTGG' | TTAG | CA T | TTGT | CAGT' | r TT | ATCT' | rcag | AAA' | TTCT | CTG ' | TGAT' | raaga. | A 530 |
| GAT | AATT | TAT ' | TAAA | GGTG | GT C | CTTC | CTAC | C TC | rg t g | GTGT | GTG' | TCGC | GCA (| CACA | GCTTA | G 590 |
| AAG | rgcti | ATA . | AAAA | AGGA | AA G | AGCT | CCAA | A TT | GAAT | CACC | TTA' | TAAT' | TTA · | CCCA' | TTTCT. | A 650 |
| TAC | AACA | GGC . | AGTG | GAAG | CA G | TTTC | GAGA | C TT | TTTC | GATG | CTT | ATGG' | TTG . | ATCA | GTTAA | A 710 |
| ΔΔΔα | 3 ል ውጥ | ታ ጥጥ | ACAG | таас | י ב ב ב | מממד | GTGC: | Α GT′ | TTAA | Δ | | | | | | 747 |

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 90 amino acids(B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile 65 70 75 80

Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly 85 90

(2) INFORMATION FOR SEQ ID NO: 13:

| (i) SEQU | JENCE | CHARAC | TERIS | TICS: |
|----------|-------|--------|-------|-------|
|----------|-------|--------|-------|-------|

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION:1..291
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide (B) LOCATION:1..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

| • | • |
|---|-----|
| ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15 | 48 |
| TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 · 25 30 | 96 |
| AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45 | 144 |
| ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GTC TGG GGA GAA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys 50 60 | 192 |
| AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 65 70 75 80 | 240 |
| AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 85 90 95 | 288 |
| AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys | 341 |
| TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG | 401 |
| GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT | 461 |
| ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC | 521 |
| TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT | 581 |
| GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT | 641 |
| TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT | 701 |
| TTAAA | 706 |

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
|-----------|-----------|-----------|-------------------------|--|-----------------------|-----------------------|-----------------------|---------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----|
| Ser | Gly | Ser | Ser 20 | Gly | Ser | Lys | Ser | Gly 25 | Gly | Asp | Lys | Met | Phe 30 | Ser | Leu | |
| Lys | Lys | Trp 35 | Asn | Ala | Val | Ala | Met 40 | Trp | Ser | Trp | Asp | Val 45 | Glu | Cys | Asp | |
| Thr | Cys 50 | Ala | Ile | Суѕ | Arg | Val 55 | Gln | Val | Met | Val | Val 60 | Trp | Gly | Glu | Cys | |
| Asn 65 | His | Ser | Phe | His | Asn 70 | Cys | Cys | Met | Ser | Leu 75 | Trp | Val | Lys | Gln | Asn 80 | |
| Asn | Arg | Cys | Pro | Leu 85 | Cys | Gln | Gln | Asp | Trp 90 | Val | Val | Gln | Arg | Ile 95 | Gly | |
| Lys | | | | | | | | | | | | | | | | |
| (2) | INFO | ORMA! | rion | FOR | SEQ | ID 1 | O. | 15: | | | | | | | | |
| | (i) |) SE | QUENC | CE CI | HARA | CTER: | ISTI | CS: | | | | | | | | |
| | | | | ENGTI YPE: | | | | | | | | | | | | |
| | | | | rrani POLO | | | | gle | | | | | | | | |
| | (ii) | | | | | | | ucle: | | | | | | | | |
| | | (1 | A) Di | ESCR. | IPTI | ON: | /de | sc = | "01: | ıgonı | ucle | otia | e nsa | AG. I | MT | |
| | | | | | | | | | | - | | | | | | |
| | (xi |) SE | QUEN | CE DI | ESCR: | IPTI | ON: | SEQ : | ID N | 0: 1 | 5: | | | | | |
| GCCZ | ATCTO | GCA (| GGT | CCAG | | | | | | | | | | | | 18 |
| (2) | INF | ORMA' | rion | FOR | SEQ | ID | : 07. | 16: | | | | | | | | |
| | (i) | () () | A) L1 B) T1 C) S1 | CE CI ENGTI YPE: TRANI OPOLO | H: 2' nuc DEDNI | 7 bas leic ESS: | se pa acio sino | airs d | | | | | | | | |
| | (ii) |) MOI | LECUI | LE T | YPE: | oth | er n | ucle | ic a | cid | | | - 634 | a .m | 001 " | |
| | | (2 | A) Di | ESCR: | IPTI | ON: | /de | sc = | "01: | igon | ucle | otid | e SA | 3 T.(| 02L" | |
| | | | | | | | | | | | | | | | | |
| | (xi |) SE | QUEN | CE D | ESCR: | IPTI | ON: | SEQ : | ID N | 0: 1 | 6: | | | | | |
| GGA. | CCT | CAT ' | TTGC | CGAT' | rc T | rtgg/ | AC . | | | | | | | | | 27 |
| (2) | INF | 'AMRC | TION | FOR | SEQ | ID I | NO: | 17: | | | | | | | | |
| | (i) | () () | A) LI B) T' C) S' | CE CI ENGTI YPE: TRANI OPOLO | h: 5 nuc DEDNI | 8 ba: leic ESS: | se pacionsing | airs d | | | | | | | | |
| Si | (ii | (2 | A) D | | | | | ucle: sc = | | | ucle | otid | e | | | |
| | (xi |) SEG | OHEN | CE D | ESCR | T ውጥ T | ON: | SEO | TD N | O: 1 | 7: | | | | | |

58

TTCTCCAGTG GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTCGAC

(2) INFORMATION FOR SEQ ID NO: 18:

| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
|------|-------------|---|----|
| 4 | (ii) -3" | MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX | |
| | | | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 18: | |
| ACC' | TCGGT | AT GATTTAAATG TTTACGGGCA ATTCATTTTT ATCGATGAAT TCGAGCTCG | 59 |
| (2) | INFO | RMATION FOR SEQ ID NO: 19: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) | MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5" | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 19: | |
| ттс | | TG GCAGAGAAC | 19 |
| | | RMATION FOR SEQ ID NO: 20: | |
| (2) | | SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs | |
| | | (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (ii) | MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3" | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 20: | |
| ATG | АТТТА | AA TGTTTACGGG C | 21 |
| (2) | INFO | RMATION FOR SEQ ID NO: 21: | |
| | (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (ii) | MOLECULE TYPE: cDNA | |
| | (ix) | FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1339 | |
| | (ix) | FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION:1339 | |
| | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 21: | |

| | | | | | | | | | | | | | | Ser 15 | | 40 |
|------------|---------------|-------|-------|---------------|-------|-------|---------------|-------|-------|---------------|------|-------|-------|------------------|--------|-----|
| | | | | | | | | | | | | | | TCC Ser | | 96 |
| | | | | | | | | | | | | | | TGC Cys | | 144 |
| | | | | | | | | | | | | | | AGA Arg | | 192 |
| | | | | | | | | | | | | | | GAA Glu | | 240 |
| | | | | | | | | | | | | | | CAG Gln 95 | | 288 |
| | | | | | | | | | | | | | | ATC Ile | | 336 |
| AAA Lys | TGA | GAGT(| GGT : | raga <i>i</i> | AGGC' | rt C | rtag(| CGCA | 3 TTC | GTTC <i>i</i> | AGAG | CCC | rggt | GGA | | 389 |
| TCT | rgta <i>i</i> | ATC (| CAGTO | GCCC' | ra C | AAAG | GCTA | G AAG | CACTA | ACAG | GGG | ATGAZ | ATT (| CTTC | AAATAG | 449 |
| GAG | CCGA' | rgg A | ATCTO | GTGG' | rc T | rtgg/ | ACTC | A TC | AAAG | CTT | GGT | rage? | ATT ' | TGTC | AGTTTT | 509 |
| ATC' | PTCA(| GAA A | ATTC: | rctg: | rg a | TAAC | GAAG | A TA | ATTTA | ATTA | AAG | GTGG | rcc ' | TTCC' | FACCTC | 569 |
| TGT | GGTG' | IGT (| GTCG | CGCA | CA C | AGCT: | raga <i>i</i> | A GTO | GCTA: | гааа | AAA | GGAA | AGA (| GCTC | CAAATT | 629 |
| GAA' | rcaco | CTT A | ATAA? | rtta(| cc c | ATTT(| CTAT | A CA | ACAG | GCAG | TGG | AAGC | AGT | TTCG | AGACTT | 689 |
| TTT | CGAT | GCT ? | ratgo | GTTG | AT C | AGTT | AAAA | A AG | AATG: | TAC | AGT | AACA | AAT . | AAAG' | rgcagt | 749 |
| TTA | AΑ | | | | | | | | | | | | | | | 754 |

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

100 105 110

Lys

| (2) INFORMATION FOR SEQ ID NO | 0: | 23: |
|-------------------------------|----|-----|
|-------------------------------|----|-----|

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

 - (A) NAME/KEY: CDS (B) LOCATION:1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

| ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15 | 48 |
|---|-----|
| TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30 | 96 |
| AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45 | 144 |
| ACG TGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60 | 192 |
| CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80 | 240 |
| AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95 | 288 |
| AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110 | 336 |
| AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys | 389 |
| TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG | 449 |
| GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT | 509 |
| ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC | 569 |
| TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT | 629 |
| GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT | 689 |
| TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT | 749 |
| TTAAA | 754 |

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110

Lys

- (2) INFORMATION FOR SEQ ID NO: 25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...339
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1...339
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

| ATG | GCC | GAC | GTG | GAA | GAC | GGA | GAG | GAA | ACC | TGC | GCC | CTG | GCC | TCT | CAC | 48 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Asp | Val | Glu | Asp | Gly | Glu | Glu | Thr | Cys | Ala | Leu | Ala | Ser | His | |
| 1 | | _ | | 5 | | | | | 10 | | | | | 15 | | |

| TCC | GGG | AGC | TCA | GGC | TCC | AAG | TCG | GGA | GGC | GAC | AAG | ATG | TTC | TCC | CTC | 96 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Ser | Gly | Ser | Ser | Gly | Ser | Lys | Ser | Gly | Gly | Asp | Lys | Met | Phe | Ser | Leu | |
| | _ | | 20 | | | | | 25 | | | | | 30 | | | |

| AAG AAG TGG | AAC GCG | GTG GCC | ATG | TGG | AGC | TGG | GAC | GTG | GAG | TGC | GAT | 144 |
|-------------|---------|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys Lys Trp | Asn Ala | Val Ala | Met | Trp | Ser | Trp | Asp | Val | Glu | Cys | Asp | |
| 35 | | | 40 | | | | | 45 | | | | |

- ACG AGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT

 Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

 50

 60
- CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT
 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80
- AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC
 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

| 3 ! | 5 9: | 0 9! | , |
|-----|------|------|---|
| | | | |

| | | /s Gln Gln | GAC TGG GTG Asp Trp Val 105 | | , Ile Gly | 336 |
|--------------------|--------------|-------------|-----------------------------------|--------------|------------|-----|
| AAA TGAGAG1 Lys | rggt tagaago | GCTT CTTAGC | GCAG TTGTTCA | AGAG CCCTGGT | PGGA | 389 |
| TCTTGTAATC | CAGTGCCCTA | CAAAGGCTAG | AACACTACAG | GGGATGAATT | CTTCAAATAG | 449 |
| GAGCCGATGG | ATCTGTGGTC | TTTGGACTCA | TCAAAGCCTT | GGTTAGCATT | TGTCAGTTTT | 509 |
| ATCTTCAGAA | ATTCTCTGTG | ATTAAGAAGA | TAATTTATTA | AAGGTGGTCC | TTCCTACCTC | 569 |
| TGTGGTGTGT | GTCGCGCACA | CAGCTTAGAA | GTGCTATAAA | AAAGGAAAGA | GCTCCAAATT | 629 |
| GAATCACCTT | ATAATTTACC | CATTTCTATA | CAACAGGCAG | TGGAAGCAGT | TTCGAGACTT | 689 |
| TTTCGATGCT | TATGGTTGAT | CAGTTAAAAA | AGAATGTTAC | AGTAACAAAT | AAAGTGCAGT | 749 |
| TTAAA | | | | | | 754 |

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 105

Lys

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 754 base pairs

 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide

(B) LOCATION: 1...339

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27: | |
|---|-----|
| ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15 | 48 |
| TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30 | 96 |
| AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45 | 144 |
| ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys 50 60 | 192 |
| CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80 | 240 |
| AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95 | 288 |
| AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110 | 336 |
| AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys | 389 |
| TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG | 449 |
| GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT | 509 |
| ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC | 569 |
| TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT | 629 |
| GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT | 689 |
| TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT | 749 |
| TTAAA | 754 |

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

| Asn | His | Ser | Phe | His 85 | Asn | Cys | Cys | Met | Ser 90 | Leu | Trp | Val | Lys | Gln 95 | Asn | |
|------------|------------------|-------------------|-------------------------|-------------------------|----------------------------|-----------------------|-----------------------|-------------------|------------|------------|------------|------------|-------------------|---------------|--------------|-----|
| Asn | Arg | Cys | Pro 100 | Leu | Cys | Gln | Gln | Asp 105 | Trp | Val | Val | Gln | Arg 110 | Ile | Gly | |
| Lys | | | | | | | | | | | | | | | | |
| (2) | INFO | ORMA | rion | FOR | SEQ | ID 1 | 10: 2 | 29: | | | | | | | | |
| | (i) | () () () | A) LI B) T' C) S' | ENGTI YPE : FRANI | HARACH: 75 nuc: DEDNI DGY: | 54 ba leic ESS: | ase p acid doul | pairs i | 5 | | | | | | | |
| | (ii) | MOI | LECUI | LE T | YPE: | CDNA | A | | | | | | | | | |
| | (ix) | (2 | | AME/I | KEY: ION: 1 | | 39 | | | | | | | | | |
| | (ix) | (2 | | AME/I | KEY: ION: | | | tide | | | | | | | | |
| | (xi |) SE | QUEN | CE DI | ESCR | IPTI | ON: | SEQ : | ID NO | 0: 29 | ∍: | | | | | |
| | GCC Ala | | | | | | | | | | | | | | | 48 |
| | GGG Gly | | | | | | | | | | | | | | | 96 |
| | AAG Lys | | | | | | | | | | | | | | | 144 |
| | TGC Cys 50 | | | | | | | | | | | | | | | 192 |
| | GCT Ala | | | | | | | | | | | | | | | 240 |
| | CAT His | | | | | | | | | | | | | | | 288 |
| AAT Asn | CGC Arg | TGC Cys | CCT Pro 100 | CTC Leu | TGC Cys | CAG Gln | CAG Gln | GAC Asp 105 | TGG Trp | GTG Val | GTC Val | CAA Gln | AGA Arg 110 | ATC Ile | GGC Gly | 336 |
| AAA Lys | TGA | GAGT | GGT ' | TAGA | AGGC' | гт С' | rtag: | CGCA | G TT(| GTTC | AGAG | CCC' | rggt(| GGA | | 389 |
| TCT | TGTA | ATC (| CAGT | GCCC' | TA C | AAAG | GCTA | G AA | CACT | ACAG | GGG | ATGA | ATT (| CTTC | AAATAG | 449 |
| GAG | CCGA' | rgg : | ATCT | GTGG' | TC T | TTGG | ACTC | A TC | AAAG | CCTT | GGT | rage. | ATT ' | TGTC | AGTTTT | 509 |
| ATC | TTCA | GAA 2 | ATTC' | TCTG' | TG A' | TTAA | GAAG. | A TA | ATTT | ATTA | AAG | GTGG' | rcc ' | TTCC | TACCTC | 569 |
| TGT | GGTG' | rgt (| GTCG | CGCA | CA C | AGCT' | TAGA. | A GT | GCTA' | TAAA | AAA | GGAA. | AGA (| GCTC | CAAATT | 629 |
| C N N | m | nm. | אתאאו | א מחוחים | 00 0 | א תיתיתיי | ייי ע ייי | 7 C7 | አሮአር | CAC | TCC | AACC | ልርጥ ' | ም ሞርር: | מב א כי יידי | 689 |

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT

754 TTAAA

| (2) INFORMATION FOR SEQ ID NO: 3 | (2) | INFORMATION | FOR | SEO | ID | NO: | 30 |
|----------------------------------|-----|-------------|-----|-----|----|-----|----|
|----------------------------------|-----|-------------|-----|-----|----|-----|----|

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

| ATG | GCC | GAC | GTG | GAA | GAC | GGA | GAG | GAA | ACC | TGC | GCC | CTG | GCC | TCT | CAC | 48 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Asp | Val | Glu | Asp | Gly | Glu | Glu | Thr | Cys | Ala | Leu | Ala | Ser | His | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

- TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
- AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 144
- ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
- CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240

| G1n 65 | Ala | Glu | Asn | Lys | Gln 70 | Glu | Asp | Cys | Val | Val 75 | Val | Trp | Gly | Glu | Cys 80 | |
|------------|-------|-------|-------------------|---------------|-----------|-------|---------------|-------|-------|-----------|------|---------------|-------|-------|------------|-----|
| | | | TTC Phe | | | | | | | | | | | | | 288 |
| | | | CCT Pro 100 | | | | | | | | | | | | GGC Gly | 336 |
| AAA Lys | TGAC | SAGT | GGT 1 | ΓAGA <i>I</i> | AGGC" | rt Ci | rtag(| CGCA | TTC | GTTC? | AGAG | ccc | rggto | GGA | | 389 |
| TCTT | GTA? | ATC (| CAGTO | GCCCI | ra ca | AAAGO | CTAC | AA(| CACTA | ACAG | GGG | ATGA | ATT (| CTTC | AAATAG | 449 |
| GAG | CCGAT | rgg 2 | ATCTO | STGGT | C T | rtgg | ACTC | A TC | AAAGO | CCTT | GGT | ragc <i>i</i> | ATT ' | rgrc? | AGTTTT | 509 |
| ATC | TCAC | SAA A | ATTCI | rctg: | rg Ar | rtaa(| GAAGA | A TAZ | \TTT? | ATTA | AAG | GTGG' | rcc ' | TTCC: | TACCTC | 569 |
| TGT | GTGT | GT (| GTCGC | CGCA | CA CA | AGCTT | raga <i>i</i> | A GTO | GCTAT | LAAA | AAA | GAA | AGA (| GCTC | CAAATT | 629 |
| GAAT | CACC | CTT A | ATAAT | TTTA(| CC CZ | ATTT(| TATA | A CA | ACAGO | GCAG | TGG | AAGC | AGT ' | rtcg/ | AGACTT | 689 |
| TTTC | CGATO | GCT 1 | ratg(| GTTG# | AT C | AGTT | XAAA! | A AG | AATGT | TAC | AGT | AACA | AAT A | AAAG' | rgcagt | 749 |
| TTA | AΑ | | | | | | | | | | | | | | | 754 |

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1...339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

| | | | - | | | | | | | | | | | | | |
|------------------|---------------|------------|-------------------|------------------|------------------|------------|------------|-------------------|------------------|------------------|------------|------------|-------------------|------------------|------------------|-----|
| | | | | | | | | | | | | | | TCT Ser 15 | | 48 |
| | | | | | | | | | | | | | | TCC Ser | | 96 |
| | | | | | | | | | | | | | | TGC Cys | | 144 |
| | | | | | | | | | | | | | | AGA Arg | | 192 |
| CAA Gln 65 | GCT Ala | GAA Glu | AAC Asn | AAA Lys | CAA Gln 70 | GAG Glu | GAC Asp | TGT Cys | GTT Val | GTG Val 75 | GTC Val | TGG Trp | GGA Gly | GAA Glu | TGT Cys 80 | 240 |
| AAT Asn | CAT His | TCC Ser | TTC Phe | AAG Lys 85 | AAC Asn | TGC Cys | TGC Cys | ATG Met | TCC Ser 90 | CTG Leu | TGG Trp | GTG Val | AAA Lys | CAG Gln 95 | AAC Asn | 288 |
| AAT Asn | CGC Arg | TGC Cys | CCT Pro 100 | CTC Leu | TGC Cys | CAG Gln | CAG Gln | GAC Asp 105 | TGG Trp | GTG Val | GTC Val | CAA Gln | AGA Arg 110 | ATC Ile | GGC Gly | 336 |
| AAA Lys | TGAG | GAGT | GGT ' | TAGA | AGGC' | TT C | rtag(| CGCA | G TT | GTTC | AGAG | CCC′ | rggt(| GGA | | 389 |
| TCT | rgta <i>i</i> | ATC (| CAGT | GCCC' | ra C | AAAG | GCTA | G AAG | CACT | ACAG | GGG | ATGA | TTA | CTTC | AAATAG | 449 |
| GAG | CCGA | rgg 2 | ATCT | GTGG' | TC T | TTGG | ACTC | A TC | AAAG | ССТТ | GGT' | TAGC. | ATT ' | TGTC | AGTTTT | 509 |
| ATC | TTCA | GAA A | ATTC' | TCTG' | rg A | TTAA | GAAG | A TA | ATTT. | ATTA | AAG | GTGG' | TCC ' | TTCC' | TACCTC | 569 |
| TGT | GGTG | rgt (| GTCG(| CGCA | CA C | AGCT" | raga. | A GT | GCTA' | TAAA | AAA | GGAA. | AGA (| GCTC | CAAATT | 629 |
| GAA' | rcaco | CTT A | ATAA' | TTTA | cc c | ATTT | CTAT | A CA | ACAG | GCAG | TGG. | AAGC. | AGT ' | TTCG | AGACTT | 689 |
| TTT | CGAT | GCT ' | TATG(| GTTG. | AT C | AGTT | AAAA | A AG | AATG' | TTAC | AGT. | AACA. | AAT . | AAAG' | TGCAGT | 749 |
| TTA | AA | | | | | | | | | | | | | | | 754 |

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp $35 \hspace{1cm} 40 \hspace{1cm} 45$

| Thr | Cys 50 | Ala | Ile | Суѕ | Arg | Val 55 | Gln | Val | Met | Asp | Ala 60 | Cys | Leu | Arg | Cys | |
|------------|------------------|------------|-------------------------|------------------------|---|-----------------------|-----------------------|-------------------|------------|------------------|------------------|------------|-------------------|------------|------------|-------|
| Gln 65 | Ala | Glu | Asn | Lys | Gln 70 | Glu | Asp | Cys | Val | Val 75 | Val | Trp | Gly | Glu | Cys 80 | |
| Asn | His | Ser | Phe | Lys 85 | Asn | Cys | Cys | Met | Ser 90 | Leu | Trp | Val | Lys | Gln 95 | Asn | |
| Asn | Arg | Cys | Pro 100 | Leu | Cys | Gln | Gln | Asp 105 | Trp | Val | Val | Gln | Arg 110 | Ile | Gly | |
| Lys | | | | | | | | | | | | | | | | |
| (2) | INF | ORMAT | rion | FOR | SEQ | ID I | 10: 3 | 35: | | | | | | | | |
| | (i) | (I (C | A) LI 3) TY C) ST | ENGTI PE : PRANI | HARAG H: 75 nucl DEDNI DGY: | 54 ba leic ESS: | ase p acio doul | pair: | 5 | | | | | | | |
| | (ii) | MOI | LECUI | LE T | PE: | CDN | A | | | | | | | | | |
| | (ix) | - | A) N2 | AME/I | KEY: ION: 1 | | 39 | | | | | | | | | |
| | (ix) | | A) NA | AME/I | KEY: | | | tide | | | | | | | | |
| | (xi |) SE(| QUEN | CE DI | ESCR | IPTI | ON: | SEQ : | ID NO | D: 35 | 5: | | | | | |
| | | | | | | | | | | TGC Cys | | | | | | 48 |
| | | | | | | | | | | GAC Asp | | | | | | 96 |
| | | | | | | | | | | TGG Trp | | | | | | 144 |
| ACG Thr | TGC Cys 50 | GCC Ala | ATC Ile | TGC Cys | AGG Arg | GTC Val 55 | CAG Gln | GTG Val | ATG Met | . GAT Asp | GCC Ala 60 | TGT Cys | CTT Leu | AGA Arg | TGT Cys | 192 |
| | | | | | | | | | | GTG Val 75 | | | | | | 240 |
| | | | | | | | | | | CTG Leu | | | | | | 288 |
| AAT Asn | CGC Arg | TGC Cys | CCT Pro 100 | CTC Leu | TGC Cys | CAG Gln | CAG Gln | GAC Asp 105 | TGG Trp | GTG Val | GTC Val | CAA Gln | AGA Arg 110 | ATC Ile | GGC Gly | 336 |
| AAA Lys | TGA | GAGT | GGT ' | TAGA | AGGC' | гт С | rtag(| CGCA | G TT | GTTC | AGAG | CCC' | rggt | GGA | | 389 |
| TCT | rgta. | ATC (| CAGT | GCCC' | ra C | AAAG | GCTA | G AA | CACT | ACAG | GGG. | ATGA | ATT (| CTTC | AAATA(| G 449 |
| GAG | CCGA' | rgg 2 | ATCT | GTGG' | rc T | TTGG. | ACTC. | A TC | AAAG | CCTT | GGT' | TAGC | ATT ' | rgtc. | AGTTT | r 509 |
| | | | | | | | | | | | | | | | TACCTO | |
| ጥርጥር | 2CTC' | ኮርጥ (| ጌጥ ርርር | CCCA | CAC | ልርርጥ | TAGA | A GT(| CCTA | ΔΔΔΤ | AAA | GGAA | AGA (| 3CTC | CAAAT | r 629 |

| TTAAA | 754 |
|---|-----|
| | |
| (2) INFORMATION FOR SEQ ID NO: 36: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 113 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36: | |
| Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15 | |
| Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30 | |
| Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45 | |
| Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60 | |
| Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80 | |
| Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn 85 90 95 | |
| Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110 | |
| Lys | |
| (2) INFORMATION FOR SEQ ID NO: 37: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: cDNA | |
| (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1339 | |
| <pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION:1339</pre> | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37: | |
| ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15 | 48 |
| TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30 | 96 |
| AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45 | 144 |

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT

| | | | ATC Ile | | | | | | | | | | | | | | 192 |
|------------|-------|-------|------------|---------------|-------|-------|---------------|-------|-------|---------------|------|---------------|-------|---------------|------------|---|-----|
| | | | AAC Asn | | | | | _ | - | - | | | | | | | 240 |
| | | | TTC Phe | | | | | | | | | | | | | | 288 |
| | | | | | | - | | | | | | | | | GGC Gly | | 336 |
| AAA Lys | TGAC | GAGT(| GGT T | raga <i>i</i> | AGGC" | PT CT | TTAGO | CGCAC | TT(| GTTC <i>l</i> | AGAG | CCC | rggto | GGA | | | 389 |
| тстт | 'GTA | ATC (| CAGTO | GCCC1 | ra ca | AAAGO | GCTAC | AAC | CACT | ACAG | GGGZ | ATGAZ | ATT (| CTTC | \AATAG | i | 449 |
| GAGO | CCGAT | rgg i | ATCT | GTGG: | rc T | rtgg? | ACTCA | A TC | AAAG | CCTT | GGTT | ragc <i>i</i> | ATT ! | rgtc <i>i</i> | GTTTT | ı | 509 |
| ATC | TCAC | GAA A | ATTC | rctg: | rg A | TAA(| GAAGA | A TAI | ATTT? | ATTA | AAG | GTGG | rcc ' | TTCC: | гасстс | ! | 569 |
| TGTC | GTG | rgr (| GTCG | CGCA | CA C | AGCT: | raga <i>i</i> | A GTO | GCTA? | raaa | AAA | GAA | AGA (| GCTC | CAAATT | | 629 |
| GAAT | CAC | CTT I | ATAA: | OATTI | cc cz | ATTTC | CTATA | A CA | ACAG | GCAG | TGG | AAGC | AGT ' | TTCG/ | AGACTT | ı | 689 |
| TTTC | CGATO | GCT ' | TATG | GTTG | AT C | AGTT | \AAA. | A AGA | AATG! | TTAC | AGT | AACA | AAT A | AAAG' | rgcagt | 1 | 749 |
| TTA | λA | | | | | | | | | | | | | | | | 754 |

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn $85 \hspace{1cm} 90 \hspace{1cm} 95$

Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION:1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

| | | | | | | | | | | | | | | TCT Ser 15 | | 48 |
|------------------|------------|------------|-------------------|------------------|------------------|------------|------------|-------------------|------------------|------------------|------------|------------|-------------------|------------------|------------------|-----|
| | | | | | | | | | | | | | | TCC Ser | | 96 |
| | | | | | | | | | | | | | | TGC Cys | | 144 |
| | | | | | | | | | | | | | | AGA Arg | | 192 |
| CAA Gln 65 | GCT Ala | GAA Glu | AAC Asn | AAA Lys | CAA Gln 70 | GAG Glu | GAC Asp | TGT Cys | GTT Val | GTG Val 75 | GTC Val | TGG Trp | GGA Gly | GAA Glu | TGT Cys 80 | 240 |
| AAT Asn | AAA Lys | TCC Ser | TTC Phe | AAG Lys 85 | AAC Asn | TGC Cys | TGC Cys | ATG Met | TCC Ser 90 | CTG Leu | TGG Trp | GTG Val | AAA Lys | CAG Gln 95 | AAC Asn | 288 |
| AAT Asn | CGC Arg | TGC Cys | CCT Pro 100 | CTC Leu | TGC Cys | CAG Gln | CAG Gln | GAC Asp 105 | TGG Trp | GTG Val | GTC Val | CAA Gln | AGA Arg 110 | ATC Ile | GGC Gly | 336 |
| AAA Lys | TGA | GAGT | GGT ' | raga | AGGC' | rt C | rtag(| CGCA | G TTC | GTTC | AGAG | CCC | rggt | GGA | | 389 |
| TCTT | rgta. | ATC (| CAGT | GCCC' | ra c | AAAG | GCTA(| G AAG | CACT | ACAG | GGG | ATGA | ATT (| CTTC | AAATAG | 449 |
| GAGO | CCGA | rgg 2 | ATCT | GTGG' | rc T | rtgg: | ACTC | A TC | AAAG | ССТТ | GGT' | rage. | ATT ' | rgrc2 | AGTTTT | 509 |
| ATCT | rtca | GAA 2 | ATTC' | TCTG' | rg A' | TTAA | GAAG | A TA | ATTT | ATTA | AAG | GTGG' | rcc ' | TTCC' | FACCTC | 569 |
| TGTO | GTG | rgr (| GTCG | CGCA | CA C | AGCT' | raga. | A GT | GCTA' | TAAA | AAA | GGAA | AGA (| GCTC | CAAATT | 629 |
| GAA' | rcac | CTT A | ATAA' | TTTA | cc c | ATTT | CTAT | A CA | ACAG | GCAG | TGG | AAGC | AGT ' | TTCG | AGACTT | 689 |
| TTTC | CGAT | GCT 1 | ratg(| GTTG. | AT C | AGTT | AAAA | A AG | AATG' | TTAC | AGT | AACA | AAT . | AAAG' | rgcagt | 749 |
| TTA | AA | | | | | | | | | | | | | | | 754 |

- (2) INFORMATION FOR SEQ ID NO: 40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 - (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 45Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80 Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

| | | | | | GAC Asp | | | | | | | | | | | 48. |
|------------------|------------|------------|------------|---------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|-----|
| | | | | | TCC Ser | | | | | | | | | | | 96 |
| | | | | | GTG Val | | | | | | | | | | | 144 |
| | | | | | AGG Arg | | | | | | | | | | | 192 |
| CAA Gln 65 | GCT Ala | GAA Glu | AAC Asn | AAA Lys | CAA Gln 70 | GAG Glu | GAC Asp | TGT Cys | GTT Val | GTG Val 75 | GTC Val | TGG Trp | GGA Gly | GAA Glu | TGT Cys 80 | 240 |
| | | | | | AAC Asn | | | | | | | | | | | 288 |
| | | | | | TGC Cys | | | | | | | | | | | 336 |
| AAA Lys | TGAG | GAGT | GGT 7 | raga <i>i</i> | AGGC' | rr C | rtag(| CGCA | TT(| GTTC | AGAG | CCC | rggt | GGA | | 389 |

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG

| GAGCCGATGG ATCTGTGGTC | TTTGGACTCA | TCAAAGCCTT | GGTTAGCATT | TGTCAGTTTT | 509 |
|-----------------------|------------|------------|------------|------------|-----|
| ATCTTCAGAA ATTCTCTGTG | ATTAAGAAGA | TAATTTATTA | AAGGTGGTCC | TTCCTACCTC | 569 |
| TGTGGTGTGT GTCGCGCACA | CAGCTTAGAA | GTGCTATAAA | AAAGGAAAGA | GCTCCAAATT | 629 |
| GAATCACCTT ATAATTTACC | САТТТСТАТА | CAACAGGCAG | TGGAAGCAGT | TTCGAGACTT | 689 |
| TTTCGATGCT TATGGTTGAT | CAGTTAAAAA | AGAATGTTAC | AGTAACAAAT | AAAGTGCAGT | 749 |
| TTAAA | | | | | 754 |
| | | | | | |

- (2) INFORMATION FOR SEQ ID NO: 42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp $35 \hspace{1cm} 40 \hspace{1cm} 45$

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 105

Lys

- (2) INFORMATION FOR SEQ ID NO: 43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1...339
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

| ATG | GCC | GAC | GTG | GAA | GAC | GGA | GAG | GAA | ACC | TGC | GCC | CTG | GCC | TCT | CAC | 48 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Asp | Val | Glu | Asp | Gly | Glu | Glu | Thr | Cys | Ala | Leu | Ala | Ser | His | |
| 1 | | _ | | 5 | | | | | 10 | | | | | 15 | | |

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

| | | | | | | | | | | | | | | TGC Cys | | 144 |
|------------|------|-------|-------|---------------|-------|-------|-------|-------|-------|---------------|------|---------------|-------|------------------|------------|-----|
| | | | | | | | | | | | | | | AGA Arg | | 192 |
| | | | | | | | | | | | | | | GAA Glu | | 240 |
| | | | | | | | | | | | | | | CAG Gln 95 | | 288 |
| | | | | | | | | | | | | | | ATC Ile | GGC Gly | 336 |
| AAA Lys | TGAC | GAGT | GGT T | ΓAGA <i>!</i> | AGGC' | rt C | rtag(| CGCA | G TTC | GTTC <i>i</i> | AGAG | ccci | rggt | GGA | | 389 |
| тстт | GTA | ATC (| CAGTO | GCCC' | ra ca | AAAG | GCTAC | AA G | CACTA | ACAG | GGG | ATGAZ | ATT (| CTTC | AAATAG | 449 |
| GAGC | CGAT | rgg i | ATCTO | GTGG1 | rc T | rtgg/ | ACTC | A TC | AAAG | ССТТ | GGT | ragc <i>i</i> | ATT ' | rgtc <i>i</i> | AGTTTT | 509 |
| ATCI | TCAC | GAA A | ATTCI | rctg? | rg ar |)AATI | GAAGA | A TA | ATTT? | ATTA | AAGO | GTGG: | rcc ' | TTCC | PACCTC | 569 |
| TGTC | GTGT | rgt (| GTCG | CGCAC | CA CA | AGCT | ragà. | A GTO | GCTA | ГААА | AAAC | GAAZ | AGA (| GCTC | CAAATT | 629 |
| GAAI | CAC | CTT A | ATAAT | PTTA(| CC CZ | ATTT(| CTATA | A CA | ACAG | GCAG | TGG | AAGC | AGT ' | TTCG | GACTT | 689 |
| TTTC | GAT | GCT ' | TATGO | GTTG <i>I</i> | AT C | AGTT | AAAA | A AG | AATG | TAC | AGT | AACA | AAT . | AAAG: | rgcagt | 749 |
| TTAA | λA | | | | | | | | | | | | | | | 754 |

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp \$35\$

Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 45:

| / ÷ \ | CECTENICE | CHARACTERISTICS: |
|-------|-----------|------------------|
| | SECUENCE | CHARACIENISIICS: |

- SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 754 base pairs

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: double

 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION:1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

| | ,, | | - | | | | | ~ | | | | | | | | | |
|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|---|-----|
| | GCC Ala | | | | | | | | | | | | | | | | 48 |
| TCC Ser | GGG Gly | AGC Ser | TCA Ser 20 | GGC Gly | TCC Ser | AAG Lys | TCG Ser | GGA Gly 25 | GGC Gly | GAC Asp | AAG Lys | ATG Met | TTC Phe 30 | TCC Ser | CTC Leu | | 96 |
| AAG Lys | AAG Lys | TGG Trp 35 | AAC Asn | GCG Ala | GTG Val | GCC Ala | ATG Met 40 | TGG Trp | AGC Ser | TGG Trp | GAC Asp | GTG Val 45 | GAG Glu | TGC Cys | GAT Asp | | 144 |
| ACG Thr | TGC Cys 50 | GCC Ala | ATC Ile | TGC Cys | AGG Arg | GTC Val 55 | CAG Gln | GTG Val | ATG Met | GAT Asp | GCC Ala 60 | AGT Ser | CTT Leu | AGA Arg | AGT Ser | | 192 |
| CAA Gln 65 | GCT Ala | GAA Glu | AAC Asn | AAA Lys | CAA Gln 70 | GAG Glu | GAC Asp | TGT Cys | GTT Val | GTG Val 75 | GTC Val | TGG Trp | GGA Gly | GAA Glu | TGT Cys 80 | | 240 |
| AAT Asn | CAT His | TCC Ser | TTC Phe | CAC His 85 | AAC Asn | TGC Cys | TGC Cys | ATG Met | TCC Ser 90 | CTG Leu | TGG Trp | GTG Val | AAA Lys | CAG Gln 95 | AAC Asn | | 288 |
| AAT Asn | CGC Arg | TGC Cys | CCT Pro 100 | CTC Leu | TGC Cys | CAG Gln | CAG Gln | GAC Asp 105 | TGG Trp | GTG Val | GTC Val | CAA Gln | AGA Arg 110 | ATC Ile | GGC Gly | | 336 |
| AAA Lys | TGA | GAGT | GGT ' | TAGA. | AGGC' | TT C | rtag(| CGCA | G TT | GTTC | AGAG | CCC' | rggT(| GGA | | | 389 |
| тст | TGTA | ATC (| CAGT | GCCC | TA C | AAAG | GCTA | G AA | CACT | ACAG | GGG. | ATGA | ATT (| CTTC | AAATAG | | 449 |
| GAG | CCGA' | TGG . | ATCT | GTGG | TC T | TTGG | ACTC | A TC | AAAG | CCTT | GGT | TAGC | ATT ' | TGTC | AGTTTT | | 509 |
| ATC | TTCA | GAA 2 | ATTC' | TCTG | TG A | TTAA | GAAG. | A TA | ATTT | АТТА | AAG | GTGG' | rcc ' | TTCC | TACCTC | | 569 |
| TGT | GGTG' | TGT (| GTCG | CGCA | CA C | AGCT' | TAGA | A GT | GCTA' | TAAA | AAA | GGAA. | AGA (| GCTC | САААТТ | | 629 |
| GAA | TCAC | CTT . | ATAA' | TTTA | CC C. | ATTT | CTAT. | A CA | ACAG | GCAG | TGG. | AAGC. | AGT ' | TTCG | AGACTT | ı | 689 |
| TTT | CGAT | GCT ' | TATG | GTTG | AT C | AGTT. | AAAA | A AG | AATG' | TTAC | AGT. | AACA | AAT . | AAAG' | TGCAGT | 1 | 749 |
| TTA | AA | | | | | | | | | | | | | | | | 754 |
| | | | | | | | | | | | | | | | | | |

- (2) INFORMATION FOR SEQ ID NO: 46:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 113 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear

 - (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

| Met 1 | Ala | Asp | Val | Glu 5 | Asp | Gly | Glu | Glu | Thr 10 | Cys | Ala | Leu | Ala | Ser 15 | His | |
|---|---|------------------|------------|-----------------|------------------|------------|------------------|------------|------------------|------------------|------------|------------------|------------|------------------|------------------|-----|
| Ser | Gly | Ser | Ser 20 | Gly | Ser | Lys . | Ser | Gly 25 | Gly | Asp | Lys | Met | Phe 30 | Ser | Leu | |
| Lys | Lys | Trp 35 | Asn | Ala | Val | Ala | Met 40 | Trp | Ser | Trp | qaA | Val 45 | Glu | Cys | Asp | |
| Thr | Cys 50 | Ala | Ile | Cys | Arg | Val 55 | Gln | Val | Met | Asp | Ala 60 | Ser | Leu | Arg | Ser | |
| Gln 65 | Ala | Glu | Asn | Lys | Gln 70 | Glu | Asp | Cys | Val | Val 75 | Val | Trp | Gly | Glu | Cys 80 | |
| Asn | His | Ser | Phe | His 85 | Asn | Cys | Cys | Met | Ser 90 | Leu | Trp | Val | Lys | Gln 95 | Asn | |
| Asn | Arg | Cys | Pro 100 | Leu | Cys | Gln | Gln | Asp 105 | Trp | Val | Val | Gln | Arg 110 | Ile | Gly | |
| Lys | | | | | | | | | | | | | | | | |
| (2) | INF | ORMAT | NOI | FOR | SEQ | ID N | VO: 4 | 17: | | | | | | | | |
| (2) INFORMATION FOR SEQ ID NO: 47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | | | | | | | | | | | | | | |
| | (ii) MOLECULE TYPE: cDNA | | | | | | | | | | | | | | | |
| (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1339 | | | | | | | | | | | | | | | | |
| <pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION:1339</pre> | | | | | | | | | | | | | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47: | | | | | | | | | | | | | | | |
| ATG Met 1 | GCC Ala | GAC Asp | GTG Val | GAA Glu 5 | GAC Asp | GGA Gly | GAG Glu | GAA Glu | ACC Thr 10 | TGC Cys | GCC Ala | CTG Leu | GCC Ala | TCT Ser 15 | CAC His | 48 |
| | | AGC Ser | | | | | | | | | | | | | | 96 |
| AAG Lys | AAG Lys | TGG Trp 35 | Asn | GCG Ala | GTG Val | GCC Ala | ATG Met 40 | TGG Trp | AGC Ser | TGG Trp | GAC Asp | GTG Val 45 | GAG Glu | TGC Cys | GAT Asp | 144 |
| | | GCC Ala | | | | | | | | | | | | | | 192 |
| CAA Gln 65 | GCT Ala | GAA Glu | AAC Asn | AAA Lys | CAA Gln 70 | GAG Glu | GAC Asp | TGT Cys | GTT Val | GTG Val 75 | GTC Val | TGG Trp | GGA Gly | GAA Glu | TGT Cys 80 | 240 |
| | | TCC Ser | | | | | | | | | | | | | | 288 |
| | | AGC Ser | | | | | | | | | | | | | | 336 |

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA

| TTAAA | | | | | | 754 |
|------------|------------|------------|------------|------------|------------|-----|
| TTTCGATGCT | TATGGTTGAT | CAGTTAAAAA | AGAATGTTAC | AGTAACAAAT | AAAGTGCAGT | 749 |
| GAATCACCTT | ATAATTTACC | CATTTCTATA | CAACAGGCAG | TGGAAGCAGT | TTCGAGACTT | 689 |
| TGTGGTGTGT | GTCGCGCACA | CAGCTTAGAA | GTGCTATAAA | AAAGGAAAGA | GCTCCAAATT | 629 |
| ATCTTCAGAA | ATTCTCTGTG | ATTAAGAAGA | ТААТТТАТТА | AAGGTGGTCC | TTCCTACCTC | 569 |
| GAGCCGATGG | ATCTGTGGTC | TTTGGACTCA | TCAAAGCCTT | GGTTAGCATT | TGTCAGTTTT | 509 |
| TCTTGTAATC | CAGTGCCCTA | CAAAGGCTAG | AACACTACAG | GGGATGAATT | CTTCAAATAG | 449 |

- (2) INFORMATION FOR SEQ ID NO: 48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100

Lys

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
|---|------------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|------------|---|-----|
| TCC Ser | GGG Gly | AGC Ser | TCA Ser 20 | GGC Gly | TCC Ser | AAG Lys | TCG Ser | GGA Gly 25 | GGC Gly | GAC Asp | AAG Lys | ATG Met | TTC Phe 30 | TCC Ser | CTC Leu | | 96 |
| AAG Lys | AAG Lys | TGG Trp 35 | AAC Asn | GCG Ala | GTG Val | GCC Ala | ATG Met 40 | TGG Trp | AGC Ser | TGG Trp | GAC Asp | GTG Val 45 | GAG Glu | AGC Ser | GAT Asp | : | 144 |
| ACG Thr | TGC Cys 50 | GCC Ala | ATC Ile | TGC Cys | AGG Arg | GTC Val 55 | CAG Gln | GTG Val | ATG Met | GAT Asp | GCC Ala 60 | TGT Cys | CTT Leu | AGA Arg | TGT Cys | : | 192 |
| | | | | | | | | | | | | | | GAA Glu | | : | 240 |
| AAT Asn | CAT His | TCC Ser | TTC Phe | CAC His 85 | AAC Asn | TGC Cys | TGC Cys | ATG Met | TCC Ser 90 | CTG Leu | TGG Trp | GTG Val | AAA Lys | CAG Gln 95 | AAC Asn | : | 288 |
| | | | | | | | | | | | | | | ATC Ile | | : | 336 |
| AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys | | | | | | | | | | | | | 389 | | | | |
| TCT: | rgta <i>i</i> | ATC (| CAGT | GCCC' | ra c | AAAG | GCTA(| G AAG | CACT | ACAG | GGG | ATGAZ | ATT (| CTTC | AAATAG | ; | 449 |
| GAG | CCGAT | rgg i | ATCT | GTGG | rc T | rtgg2 | ACTC | A TC | AAAG | CCTT | GGT | ragc2 | ATT ' | TGTC | AGTTTT | ı | 509 |
| ATC | rtca(| GAA A | ATTC' | TCTG' | rg a | TAA(| GAAG | A TA | ATTT | ATTA | AAG | GTGG' | rcc ' | TTCC | PACCTC | ! | 569 |
| TGT | GGTGT | rgt (| GTCG | CGCA | CA C | AGCT' | raga <i>i</i> | A GT | GCTA' | TAAA | AAA | GGAA | AGA (| GCTC | CAAATT | , | 629 |
| GAA' | rcac(| CTT A | ATAA' | TTTA | CC C | ATTT | CTAT | A CA | ACAG | GCAG | ŢGG | AAGC | AGT ' | TTCG | AGACTT | 1 | 689 |
| TTTC | CGATO | GCT ' | TATG | GTTG | AT C | AGTT | AAAA | A AG | AATG' | TTAC | AGT | AACA | AAT . | AAAG' | rgcagt | 3 | 749 |
| TTA | AA | | | | | | | | | | | | | | | | 754 |
| | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95 .

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 $$ 105 $$ 110

Cont Lys